

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/581,008  
Source: IFWP  
Date Processed by STIC: 6/9/06

***ENTERED***



IFWP

## RAW SEQUENCE LISTING

DATE: 06/09/2006

PATENT APPLICATION: US/10/581,008

TIME: 10:33:34

Input Set : A:\65645(46590) sequence\_listing.txt

Output Set: N:\CRF4\06092006\J581008.raw

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3 <110> APPLICANT: Takeda Pharmaceutical Company Limited
5 <120> TITLE OF INVENTION: Method of Estimating Toxicity of Drug
7 <130> FILE REFERENCE: 09707
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/581,008
C--> 9 <141> CURRENT FILING DATE: 2006-05-26
9 <150> PRIOR APPLICATION NUMBER: JP 2003-397551
10 <151> PRIOR FILING DATE: 2003-11-27
13 <160> NUMBER OF SEQ ID NOS: 60
15 <170> SOFTWARE: PatentIn version 3.2
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 4304
19 <212> TYPE: DNA
20 <213> ORGANISM: Homo sapiens
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (459)..(2033)
27 <400> SEQUENCE: 1
28 gcgagaactc atcctgtagt caccagatgg agtcccaaac agccaagcag atgtaaggcc 60
30 tgtgctgtgg ctctgaggcc ctgaatacag aagggtcact ttcttagtgg ccaaagagca 120
32 gttgttgaca ttgatgtcta attattgaac acgaccagtc attttactga gctgcggtga 180
34 ggaaacactg accatagaag atcaagccaa atgagggatt gcaaatttcc tgattctttt 240
36 gaattaggat tccagatggg ggctcattt ctacagcccc caacattcct atagccgcta 300
38 tcaactgcat caccactgcc accagcatct tcttgcatat tccacccttg ctcccagag 360
40 acttctctgt ttgaaagtga gcagaaagga agctctcaga aaaatctcta gtggtggctg 420
42 ccgtcgctcc agacaatcgg aatcctgcct tcaccacc atg ggc tgg ctt ttt cta 476
43 Met Gly Trp Leu Phe Leu
44 1 5
46 aag gtt ttg ttg gcg gga gtg agt ttc tca gga ttt ctt tat cct ctt 524
47 Lys Val Leu Leu Ala Gly Val Ser Phe Ser Gly Phe Leu Tyr Pro Leu
48 10 15 20
50 gtg gat ttt tgc atc agt ggg aaa aca aga gga cag aag cca aac ttt 572
51 Val Asp Phe Cys Ile Ser Gly Lys Thr Arg Gly Gln Lys Pro Asn Phe
52 25 30 35
54 gtg att att ttg gcc gat gac atg ggg tgg ggt gac ctg gga gca aac 620
55 Val Ile Ile Leu Ala Asp Asp Met Gly Trp Gly Asp Leu Gly Ala Asn
56 40 45 50
58 tgg gca gaa aca aag gac act gcc aac ctt gat aag atg gct tcg gag 668
59 Trp Ala Glu Thr Lys Asp Thr Ala Asn Leu Asp Lys Met Ala Ser Glu
60 55 60 65 70
62 gga atg agg ttt gtg gat ttc cat gca gct gcc tcc acc tgc tca ccc 716
63 Gly Met Arg Phe Val Asp Phe His Ala Ala Ala Ser Thr Cys Ser Pro
64 75 80 85
66 tcc cgg gct tcc ttg ctc acc ggc cgg ctt ggc ctt cgc aat gga gtc 764

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67 Ser Arg Ala Ser Leu Leu Thr Gly Arg Leu Gly Leu Arg Asn Gly Val
68          90          95          100
70 aca cgc aac ttt gca gtc act tct gtg gga ggc ctt ccg ctc aac gag      812
71 Thr Arg Asn Phe Ala Val Thr Ser Val Gly Gly Leu Pro Leu Asn Glu
72          105          110          115
74 acc acc ttg gca gag gtg ctg cag cag gcg ggt tac gtc act ggg ata      860
75 Thr Thr Leu Ala Glu Val Leu Gln Gln Ala Gly Tyr Val Thr Gly Ile
76          120          125          130
78 ata ggc aaa tgg cat ctt gga cac cac ggc tct tat cac ccc aac ttc      908
79 Ile Gly Lys Trp His Leu Gly His His Gly Ser Tyr His Pro Asn Phe
80 135          140          145          150
82 cgt ggt ttt gat tac tac ttt gga atc cca tat agc cat gat atg ggc      956
83 Arg Gly Phe Asp Tyr Tyr Phe Gly Ile Pro Tyr Ser His Asp Met Gly
84          155          160          165
86 tgt act gat act cca ggc tac aac cac cct cct tgt cca gcg tgt cca      1004
87 Cys Thr Asp Thr Pro Gly Tyr Asn His Pro Pro Cys Pro Ala Cys Pro
88          170          175          180
90 cag ggt gat gga cca tca agg aac ctt caa aga gac tgt tac act gac      1052
91 Gln Gly Asp Gly Pro Ser Arg Asn Leu Gln Arg Asp Cys Tyr Thr Asp
92          185          190          195
94 gtg gcc ctc cct ctt tat gaa aac ctc aac att gtg gag cag ccg gtg      1100
95 Val Ala Leu Pro Leu Tyr Glu Asn Leu Asn Ile Val Glu Gln Pro Val
96          200          205          210
98 aac ttg agc agc ctt gcc cag aag tat gct gag aaa gca acc cag ttc      1148
99 Asn Leu Ser Ser Leu Ala Gln Lys Tyr Ala Glu Lys Ala Thr Gln Phe
100 215          220          225          230
102 atc cag cgt gca agc acc agc ggg agg ccc ttc ctg ctc tat gtg gct      1196
103 Ile Gln Arg Ala Ser Thr Ser Gly Arg Pro Phe Leu Leu Tyr Val Ala
104          235          240          245
106 ctg gcc cac atg cac gtg ccc tta cct gtg act caa cta cca gca gcg      1244
107 Leu Ala His Met His Val Pro Leu Pro Val Thr Gln Leu Pro Ala Ala
108          250          255          260
110 cca cgg ggc aga agc ctg tat ggt gca ggg ctc tgg gag atg gac agt      1292
111 Pro Arg Gly Arg Ser Leu Tyr Gly Ala Gly Leu Trp Glu Met Asp Ser
112          265          270          275
114 ctg gtg ggc cag atc aag gac aaa gtt gac cac aca gtg aag gaa aac      1340
115 Leu Val Gly Gln Ile Lys Asp Lys Val Asp His Thr Val Lys Glu Asn
116          280          285          290
118 aca ttc ctc tgg ttt aca gga gac aat ggc ccg tgg gct cag aag tgt      1388
119 Thr Phe Leu Trp Phe Thr Gly Asp Asn Gly Pro Trp Ala Gln Lys Cys
120 295          300          305          310
122 gag cta gcg ggc agt gtg ggt ccc ttc act gga ttt tgg caa act cgt      1436
123 Glu Leu Ala Gly Ser Val Gly Pro Phe Thr Gly Phe Trp Gln Thr Arg
124          315          320          325
126 caa ggg gga agt cca gcc aag cag acg acc tgg gaa gga ggg cac cgg      1484
127 Gln Gly Gly Ser Pro Ala Lys Gln Thr Thr Trp Glu Gly Gly His Arg
128          330          335          340
130 gtc cca gca ctg gct tac tgg cct ggc aga gtt cca gtt aat gtc acc      1532
131 Val Pro Ala Leu Ala Tyr Trp Pro Gly Arg Val Pro Val Asn Val Thr

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132          345          350          355
134 agc act gcc ttg tta agc gtg ctg gac att ttt cca act gtg gta gcc      1580
135 Ser Thr Ala Leu Leu Ser Val Leu Asp Ile Phe Pro Thr Val Val Ala
136          360          365          370
138 ctg gcc cag gcc agc tta cct caa gga cgg cgc ttt gat ggt gtg gac      1628
139 Leu Ala Gln Ala Ser Leu Pro Gln Gly Arg Arg Phe Asp Gly Val Asp
140 375          380          385          390
142 gtc tcc gag gtg ctg ttt ggc cgg tca cag cct ggg cac agg gtg ctg      1676
143 Val Ser Glu Val Leu Phe Gly Arg Ser Gln Pro Gly His Arg Val Leu
144          395          400          405
146 ttc cac ccc aac agc ggg gca gct gga gag ttt gga gcc ctg cag act      1724
147 Phe His Pro Asn Ser Gly Ala Ala Gly Glu Phe Gly Ala Leu Gln Thr
148          410          415          420
150 gtc cgc ctg gag cgt tac aag gcc ttc tac att acc ggt gga gcc agg      1772
151 Val Arg Leu Glu Arg Tyr Lys Ala Phe Tyr Ile Thr Gly Gly Ala Arg
152          425          430          435
154 gcg tgt gat ggg agc acg ggg cct gag ctg cag cat aag ttt cct ctg      1820
155 Ala Cys Asp Gly Ser Thr Gly Pro Glu Leu Gln His Lys Phe Pro Leu
156          440          445          450
158 att ttc aac ctg gaa gac gat acc gca gaa gct gtg ccc cta gaa aga      1868
159 Ile Phe Asn Leu Glu Asp Thr Ala Glu Ala Val Pro Leu Glu Arg
160 455          460          465          470
162 ggt ggt gcg gag tac cag gct gtg ctg ccc gag gtc aga aag gtt ctt      1916
163 Gly Gly Ala Glu Tyr Gln Ala Val Leu Pro Glu Val Arg Lys Val Leu
164          475          480          485
166 gca gac gtc ctg caa gac att gcc aac gac aac atc tcc agc cca gat      1964
167 Ala Asp Val Leu Gln Asp Ile Ala Asn Asp Asn Ile Ser Ser Pro Asp
168          490          495          500
170 tac act cag gac cct tca gta act ccc tgc tgt aat ccc tac caa att      2012
171 Tyr Thr Gln Asp Pro Ser Val Thr Pro Cys Cys Asn Pro Tyr Gln Ile
172          505          510          515
174 gcc tgc cgc tgt caa gcc gca taacagacca atttttattc cacgaggagg      2063
175 Ala Cys Arg Cys Gln Ala Ala
176          520          525
178 agtacctgga aattaggcaa gtttgcttcc aaatttccatt tttaccctct ttacaaacac      2123
180 acgcttttagt ttagtcttgg agtttagttt tggagttagc cttgcatatc ctttctgtat      2183
182 cctgtccctc ctccacgccg acccgagagc agctgagctg cgctggctct gggcagggag      2243
184 tgtgccttaa tgggaagcac acgggctttg gagtcaggca caggtgccag ctccagcttt      2303
186 tgaacttggg caattgttta acctaacctg caagttgatt ttgaggggta aataaaggca      2363
188 tacatgaaaa tgcttggaac attacctgac acagagcaga cattcaatac attttagttt      2423
190 ccttggtttct ctgggttcca gtttctctgg tcattttggt gtaaatccat tctaattagt      2483
192 atttagggca gagcttctct ctcttttctc tttttttcct tccacaaacc agtgtaactca      2543
194 ctggtctcca totttaatat gcaaacaaat cacctgggat cttgtgagaa tccggattct      2603
196 gtctcagtag ggctcgagta gatcctgaaa tctacattt ctatcaaaca atgccttgag      2663
198 gagcacagat ttagaccaa gttaggtcgt tttccagatc tcagagcaga cgagtccatg      2723
200 gataagtctg tggcccaatc ccttctctct ccttttaagg gtgaaatgac tgcatttaaa      2783
202 agaagttaaa gagttctctc tgtcccttat aaccacaagg aaacaaaaaa atatataaaa      2843
204 acctcaaaaa tgcattgcca tgattttatt attagtgtcc aaaatgggac tcccaagtaa      2903
206 taaatgattt attccagcca cagccaaaaa agactttgcc tggctaaaag agtctctctc      2963

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208 taagtatgta atatacaaga aatacaattc aaagagatgt tcctataagt acatttttta 3023
210 cacggcatat atttaaaaag gaggccctt ttaatataaa attccgggta tataccaata 3083
212 tgggtaatta gcatttacac tatagtttga acgtatttta aatagcatga tgtgtataca 3143
214 atgtctcccg cgccattgg caaccagggt cgtgggaagc ttggtagga gttaccagg 3203
216 tcctgtggtt taagcagtgg agcaccggg attcctgccc ccctttctgc tcacacaatt 3263
218 gcactccatt cttccgcctt ccttgttttc tccaaaacca cctgatagg gggatgtcct 3323
220 gatttctgag gtgtgcttct catcatgact gcttcgtttt gcccttctga tttccacggc 3383
222 acaagattat ctacaaaaat caaaacagaa tggccttact cttctcagga agaggctggt 3443
224 aggcagggtgc attatcaaca ggtctgtgcc catgcagagt gagcaggag aggctgggca 3503
226 ctgtggaatt tttctgtctg aactcgctca tggccacaga atggtcaccc agcttattta 3563
228 ggtgtagaca agtatgacac agttctagaa aatactgact ataaaaatgt ctctgtgtgt 3623
230 gtgtgtatgt atttatatgt atatgtatat atttttaaaa ggctcatctt acttgtaaac 3683
232 atggactgct caatcactat taaaaagtca gtttaggctg ggcgcggtgg ctcacgcctg 3743
234 tagtcccaga gctttgggag gctgaggtgg gtggatcact gggtcaggag tttgagacca 3803
236 gcctggccaa catggtgaaa ccccatcgct actaaaaaat acaaaaatta gccgggcatg 3863
238 gtggcgctca cctgtaatcc cggctactcg ggaggctgag gcaggagaga atcgcttgaa 3923
240 cgggggaggt ggaggctgca gtgagccgag atcgaccac tgcactccag cctgggtgat 3983
242 ggagcaagac tccatctcaa aaaaaaaaaa gtcagtttag gctgggcgca gtggctcaca 4043
244 cctgtagtcc cagcacttta ggaggctgag ggggggtgat acctgagggtc aggagtttga 4103
246 gaccagcctg gccaacatgg tgaaatcctg tctctgctaa aaatacaaaa tttagctggg 4163
248 catggtggcg tgctgaaac ccagctact tgggaggctg aggcactaga atcgcttgag 4223
250 cctgggaggt ggaggttgca gtgagtggag atcgcgccaa cacattctag cctgaggggac 4283
252 agagtggagac tctatcatct c
255 <210> SEQ ID NO: 2
256 <211> LENGTH: 525
257 <212> TYPE: PRT
258 <213> ORGANISM: Homo sapiens
260 <400> SEQUENCE: 2
262 Met Gly Trp Leu Phe Leu Lys Val Leu Leu Ala Gly Val Ser Phe Ser
263 1 5 10 15
266 Gly Phe Leu Tyr Pro Leu Val Asp Phe Cys Ile Ser Gly Lys Thr Arg
267 20 25 30
270 Gly Gln Lys Pro Asn Phe Val Ile Ile Leu Ala Asp Asp Met Gly Trp
271 35 40 45
274 Gly Asp Leu Gly Ala Asn Trp Ala Glu Thr Lys Asp Thr Ala Asn Leu
275 50 55 60
278 Asp Lys Met Ala Ser Glu Gly Met Arg Phe Val Asp Phe His Ala Ala
279 65 70 75 80
282 Ala Ser Thr Cys Ser Pro Ser Arg Ala Ser Leu Leu Thr Gly Arg Leu
283 85 90 95
286 Gly Leu Arg Asn Gly Val Thr Arg Asn Phe Ala Val Thr Ser Val Gly
287 100 105 110
290 Gly Leu Pro Leu Asn Glu Thr Thr Leu Ala Glu Val Leu Gln Gln Ala
291 115 120 125
294 Gly Tyr Val Thr Gly Ile Ile Gly Lys Trp His Leu Gly His His Gly
295 130 135 140
298 Ser Tyr His Pro Asn Phe Arg Gly Phe Asp Tyr Tyr Phe Gly Ile Pro
299 145 150 155 160
302 Tyr Ser His Asp Met Gly Cys Thr Asp Thr Pro Gly Tyr Asn His Pro

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303          165          170          175
306 Pro Cys Pro Ala Cys Pro Gln Gly Asp Gly Pro Ser Arg Asn Leu Gln
307          180          185          190
310 Arg Asp Cys Tyr Thr Asp Val Ala Leu Pro Leu Tyr Glu Asn Leu Asn
311          195          200          205
314 Ile Val Glu Gln Pro Val Asn Leu Ser Ser Leu Ala Gln Lys Tyr Ala
315          210          215          220
318 Glu Lys Ala Thr Gln Phe Ile Gln Arg Ala Ser Thr Ser Gly Arg Pro
319 225          230          235          240
322 Phe Leu Leu Tyr Val Ala Leu Ala His Met His Val Pro Leu Pro Val
323          245          250          255
326 Thr Gln Leu Pro Ala Ala Pro Arg Gly Arg Ser Leu Tyr Gly Ala Gly
327          260          265          270
330 Leu Trp Glu Met Asp Ser Leu Val Gly Gln Ile Lys Asp Lys Val Asp
331          275          280          285
334 His Thr Val Lys Glu Asn Thr Phe Leu Trp Phe Thr Gly Asp Asn Gly
335          290          295          300
338 Pro Trp Ala Gln Lys Cys Glu Leu Ala Gly Ser Val Gly Pro Phe Thr
339 305          310          315          320
342 Gly Phe Trp Gln Thr Arg Gln Gly Gly Ser Pro Ala Lys Gln Thr Thr
343          325          330          335
346 Trp Glu Gly Gly His Arg Val Pro Ala Leu Ala Tyr Trp Pro Gly Arg
347          340          345          350
350 Val Pro Val Asn Val Thr Ser Thr Ala Leu Leu Ser Val Leu Asp Ile
351          355          360          365
354 Phe Pro Thr Val Val Ala Leu Ala Gln Ala Ser Leu Pro Gln Gly Arg
355          370          375          380
358 Arg Phe Asp Gly Val Asp Val Ser Glu Val Leu Phe Gly Arg Ser Gln
359 385          390          395          400
362 Pro Gly His Arg Val Leu Phe His Pro Asn Ser Gly Ala Ala Gly Glu
363          405          410          415
366 Phe Gly Ala Leu Gln Thr Val Arg Leu Glu Arg Tyr Lys Ala Phe Tyr
367          420          425          430
370 Ile Thr Gly Gly Ala Arg Ala Cys Asp Gly Ser Thr Gly Pro Glu Leu
371          435          440          445
374 Gln His Lys Phe Pro Leu Ile Phe Asn Leu Glu Asp Asp Thr Ala Glu
375          450          455          460
378 Ala Val Pro Leu Glu Arg Gly Gly Ala Glu Tyr Gln Ala Val Leu Pro
379 465          470          475          480
382 Glu Val Arg Lys Val Leu Ala Asp Val Leu Gln Asp Ile Ala Asn Asp
383          485          490          495
386 Asn Ile Ser Ser Pro Asp Tyr Thr Gln Asp Pro Ser Val Thr Pro Cys
387          500          505          510
390 Cys Asn Pro Tyr Gln Ile Ala Cys Arg Cys Gln Ala Ala
391          515          520          525
394 <210> SEQ ID NO: 3
395 <211> LENGTH: 2258
396 <212> TYPE: DNA
397 <213> ORGANISM: Homo sapiens

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RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 06/09/2006  
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48

Seq#:49,50,51,52,53,54,55,56,57,58,59,60

VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date